



SEQUENCE LISTING

<110> Carulli, John P.
Little, Randall D.
Recker, Robert R.
Johnson, Mark L.

<120> High bone mass gene of 11q13.3

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<140> US 09/543,771

<141> 2000-04-05

<150> US 09/229,319

<151> 1999-01-13

<150> US 60/071,449

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<150> US 60/105,511

<151> 1998-10-23

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Arg Lys Val Leu Phe Trp Gln Asp Leu Asp Gln Pro Arg Ala Ile Ala
          145          150          155
ttg gac ccc gct cac ggg tac atg tac tgg aca gac tgg gtt gag acg
589
Leu Asp Pro Ala His Gly Tyr Met Tyr Trp Thr Asp Trp Val Glu Thr
          160          165          170
ccc cgg att gag cgg gca ggg atg gat ggc agc acc cgg aag atc att
637
Pro Arg Ile Glu Arg Ala Gly Met Asp Gly Ser Thr Arg Lys Ile Ile
          175          180          185
gtg gac tcg gac att tac tgg ccc aat gga ctg acc atc gac ctg gag
685
Val Asp Ser Asp Ile Tyr Trp Pro Asn Gly Leu Thr Ile Asp Leu Glu
          190          195          200          205
gag cag aag ctc tac tgg gct gac gcc aag ctc agc ttc atc cac cgt
733

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Glu Gln Lys Leu Tyr Trp Ala Asp Ala Lys Leu Ser Phe Ile His Arg
 210 215 220
 gcc aac ctg gac ggc tcg ttc cgg cag aag gtg gtg gag ggc agc ctg
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 Ala Asn Leu Asp Gly Ser Phe Arg Gln Lys Val Val Glu Gly Ser Leu
 225 230 235
 acg cac ccc ttc gcc ctg acg ctc tcc ggg gac act ctg tac tgg aca
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 Thr His Pro Phe Ala Leu Thr Leu Ser Gly Asp Thr Leu Tyr Trp Thr
 240 245 250
 gac tgg cag acc cgc tcc atc cat gcc tgc aac aag cgc act ggg ggg
 877
 Asp Trp Gln Thr Arg Ser Ile His Ala Cys Asn Lys Arg Thr Gly Gly
 255 260 265
 aag agg aag gag atc ctg agt gcc ctc tac tca ccc atg gac atc cag
 925
 Lys Arg Lys Glu Ile Leu Ser Ala Leu Tyr Ser Pro Met Asp Ile Gln
 270 275 280 285
 gtg ctg agc cag gag cgg cag cct ttc ttc cac act cgc tgt gag gag
 973
 Val Leu Ser Gln Glu Arg Gln Pro Phe Phe His Thr Arg Cys Glu Glu
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 gac aat ggc ggc tgc tcc cac ctg tgc ctg ctg tcc cca agc gag cct
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 Asp Asn Gly Gly Cys Ser His Leu Cys Leu Leu Ser Pro Ser Glu Pro
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 1069
 Phe Tyr Thr Cys Ala Cys Pro Thr Gly Val Gln Leu Gln Asp Asn Gly
 320 325 330
 agg acg tgt aag gca gga gcc gag gag gtg ctg ctg ctg gcc cgg cgg
 1117
 Arg Thr Cys Lys Ala Gly Ala Glu Glu Val Leu Leu Leu Ala Arg Arg
 335 340 345
 acg gac cta cgg agg atc tcg ctg gac acg ccg gac ttc acc gag atc
 1165
 Thr Asp Leu Arg Arg Ile Ser Leu Asp Thr Pro Asp Phe Thr Asp Ile
 350 355 360 365
 gtg ctg cag gtg gag gac atc cgg cac gcc att gcc atc gag tac gag
 1213
 Val Leu Gln Val Asp Asp Ile Arg His Ala Ile Ala Ile Asp Tyr Asp
 370 375 380
 ccg cta gag ggc tat gtc tac tgg aca gat gac gag gtg cgg gcc atc
 1261
 Pro Leu Glu Gly Tyr Val Tyr Trp Thr Asp Asp Glu Val Arg Ala Ile
 385 390 395
 cgc agg gcg tac ctg gac ggg tct ggg gcg cag acg ctg gtc aac acc
 1309
 Arg Arg Ala Tyr Leu Asp Gly Ser Gly Ala Gln Thr Leu Val Asn Thr
 400 405 410
 gag atc aac gac ccc gat ggc atc gcg gtc gac tgg gtg gcc cga aac
 1357
 Glu Ile Asn Asp Pro Asp Gly Ile Ala Val Asp Trp Val Ala Arg Asn
 415 420 425
 ctc tac tgg acc gag acg ggc acg gac cgc atc gag gtg acg cgc ctc
 1405
 Leu Tyr Trp Thr Asp Thr Gly Thr Asp Arg Ile Glu Val Thr Arg Leu

430	435										440				445		
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cga gcc atc gca ctg cac ccc gtg atg ggc ctc atg tac tgg aca gac																	
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tgg gga gag aac cct aaa atc gag tgt gcc aac ttg gat ggg cag gag																	
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	480										485				490		
cgg cgt gtg ctg gtc aat gcc tcc ctc ggg tgg ccc aac ggc ctg gcc																	
1597	Arg Arg Val Leu Val Asn Ala Ser Leu Gly Trp Pro Asn Gly Leu Ala																
	495										500				505		
ctg gac ctg cag gag ggg aag ctc tac tgg gga gac gcc aag aca gac																	
1645	Leu Asp Leu Gln Glu Gly Lys Leu Tyr Trp Gly Asp Ala Lys Thr Asp																
510	515										520				525		
aag atc gag gtg atc aat gtt gat ggg acg aag agg cgg acc ctc ctg																	
1693	Lys Ile Glu Val Ile Asn Val Asp Gly Thr Lys Arg Arg Thr Leu Leu																
	530										535				540		
gag gac aag ctc ccg cac att ttc ggg ttc acg ctg ctg ggg gac ttc																	
1741	Glu Asp Lys Leu Pro His Ile Phe Gly Phe Thr Leu Leu Gly Asp Phe																
	545										550				555		
atc tac tgg act gac tgg cag cgc cgc agc atc gag cgg gtg cac aag																	
1789	Ile Tyr Trp Thr Asp Trp Gln Arg Arg Ser Ile Glu Arg Val His Lys																
	560										565				570		
gtc aag gcc agc cgg gac gtc atc att gac cag ctg ccc gac ctg atg																	
1837	Val Lys Ala Ser Arg Asp Val Ile Ile Asp Gln Leu Pro Asp Leu Met																
	575										580				585		
ggg ctc aaa gct gtg aat gtg gcc aag gtc gtc gga acc aac ccg tgt																	
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1933	Ala Asp Arg Asn Gly Gly Cys Ser His Leu Cys Phe Phe Thr Pro His																
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gca acc cgg tgt ggc tgc ccc atc ggc ctg gag ctg ctg agt gac atg																	
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	625										630				635		
aag acc tgc atc gtg cct gag gcc ttc ttg gtc ttc acc agc aga gcc																	
2029	Lys Thr Cys Ile Val Pro Glu Ala Phe Leu Val Phe Thr Ser Arg Ala																
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gcc atc cac agg atc tcc ctc gag acc aat aac aac gac gtg gcc atc																	
2077	Ala Ile His Arg Ile Ser Leu Glu Thr Asn Asn Asn Asp Val Ala Ile																
	655										660				665		

ccg ctc acg ggc gtc aag gag gcc tca gcc ctg gac ttt gat gtg tcc
 2125
 Pro Leu Thr Gly Val Lys Glu Ala Ser Ala Leu Asp Phe Asp Val Ser
 670 675 680 685
 aac aac cac atc tac tgg aca gac gtc agc ctg aag acc atc agc cgc
 2173
 Asn Asn His Ile Tyr Trp Thr Asp Val Ser Leu Lys Thr Ile Ser Arg
 690 695 700
 gcc ttc atg aac ggg agc tcg gtg gag cac gtg gtg gag ttt ggc ctt
 2221
 Ala Phe Met Asn Gly Ser Ser Val Glu His Val Val Glu Phe Gly Leu
 705 710 715
 gac tac ccc gag ggc atg gcc gtt gac tgg atg ggc aag aac ctc tac
 2269
 Asp Tyr Pro Glu Gly Met Ala Val Asp Trp Met Gly Lys Asn Leu Tyr
 720 725 730
 tgg gcc gac act ggg acc aac aga atc gaa gtg gcg cgg ctg gac ggg
 2317
 Trp Ala Asp Thr Gly Thr Asn Arg Ile Glu Val Ala Arg Leu Asp Gly
 735 740 745
 cag ttc cgg caa gtc ctc gtg tgg agg gac ttg gac aac ccg agg tcg
 2365
 Gln Phe Arg Gln Val Leu Val Trp Arg Asp Leu Asp Asn Pro Arg Ser
 750 755 760 765
 ctg gcc ctg gat ccc acc aag ggc tac atc tac tgg acc gag tgg ggc
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 Leu Ala Leu Asp Pro Thr Lys Gly Tyr Ile Tyr Trp Thr Glu Trp Gly
 770 775 780
 ggc aag ccg agg atc gtg cgg gcc ttc atg gac ggg acc aac tgc atg
 2461
 Gly Lys Pro Arg Ile Val Arg Ala Phe Met Asp Gly Thr Asn Cys Met
 785 790 795
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 2509
 Thr Leu Val Asp Lys Val Gly Arg Ala Asn Asp Leu Thr Ile Asp Tyr
 800 805 810
 gct gac cag cgc ctc tac tgg acc gac ctg gac acc aac atg atc gag
 2557
 Ala Asp Gln Arg Leu Tyr Trp Thr Asp Leu Asp Thr Asn Met Ile Glu
 815 820 825
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 Ser Ser Asn Met Leu Gly Gln Glu Arg Val Val Ile Ala Asp Asp Leu
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 2653
 Pro His Pro Phe Gly Leu Thr Gln Tyr Ser Asp Tyr Ile Tyr Trp Thr
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 2701
 Asp Trp Asn Leu His Ser Ile Glu Arg Ala Asp Lys Thr Ser Gly Arg
 865 870 875
 aac cgc acc ctc atc cag ggc cac ctg gac ttc gtg atg gac atc ctg
 2749
 Asn Arg Thr Leu Ile Gln Gly His Leu Asp Phe Val Met Asp Ile Leu
 880 885 890
 gtg ttc cac tcc tcc cgc cag gat ggc ctc aat gac tgt atg cac aac

2797
 Val Phe His Ser Ser Arg Gln Asp Gly Leu Asn Asp Cys Met His Asn
 895 900 905
 aac ggg cag tgt ggg cag ctg tgc ctt gcc atc ccc ggc ggc cac cgc
 2845
 Asn Gly Gln Cys Gly Gln Leu Cys Leu Ala Ile Pro Gly Gly His Arg
 910 915 920 925
 tgc ggc tgc gcc tca cac tac acc ctg gac ccc agc agc cgc aac tgc
 2893
 Cys Gly Cys Ala Ser His Tyr Thr Leu Asp Pro Ser Ser Arg Asn Cys
 930 935 940
 agc ccg ccc acc acc ttc ttg ctg ttc agc cag aaa tct gcc atc agt
 2941
 Ser Pro Pro Thr Thr Phe Leu Leu Phe Ser Gln Lys Ser Ala Ile Ser
 945 950 955
 cgg atg atc ccg gac gac cag cac agc ccg gat ctc atc ctg ccc ctg
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 Arg Met Ile Pro Asp Asp Gln His Ser Pro Asp Leu Ile Leu Pro Leu
 960 965 970
 cat gga ctg agg aac gtc aaa gcc atc gac tat gac cca ctg gac aag
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 His Gly Leu Arg Asn Val Lys Ala Ile Asp Tyr Asp Pro Leu Asp Lys
 975 980 985
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 Phe Ile Tyr Trp Val Asp Gly Arg Gln Asn Ile Lys Arg Ala Lys Asp
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 3181
 Pro Asp Arg Gln Pro His Asp Leu Ser Ile Asp Ile Tyr Ser Arg Thr
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 ctg ttc tgg acg tgc gag gcc acc aat acc atc aac gtc cac agg ctg
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 Leu Phe Trp Thr Cys Glu Ala Thr Asn Thr Ile Asn Val His Arg Leu
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 Ser Gly Glu Ala Met Gly Val Val Leu Arg Gly Asp Arg Asp Lys Pro
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Val Val Asp Asn Thr Leu Gly Lys Leu Phe Trp Val Asp Ala Asp Leu
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Glu Asp Ala Asn Ile Val Gln Pro Leu Gly Leu Thr Ile Leu Gly Lys
1150 1155 1160 1165
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1170 1175 1180
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Lys Thr Thr Gly Asp Lys Arg Thr Arg Ile Gln Gly Arg Val Ala His
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3709
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3757
Ala His Pro Cys Ala Arg Asp Asn Gly Gly Cys Ser His Ile Cys Ile
1215 1220 1225
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ctc ctg cag aac ctg ctg acc tgt gga gag ccg ccc acc tgc tcc ccg
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3949
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1280 1285 1290
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3997
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Cys Val Asp Leu Arg Leu Arg Cys Asp Gly Glu Ala Asp Cys Gln Asp
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4093
Arg Ser Asp Glu Val Asp Cys Asp Ala Ile Cys Leu Pro Asn Gln Phe
1330 1335 1340
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4141
Arg Cys Ala Ser Gly Gln Cys Val Leu Ile Lys Gln Gln Cys Asp Ser

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          1345          1350          1355
    ttc ccc gac tgt atc gac ggc tcc gac gag ctc atg tgt gaa atc acc
4189
    Phe Pro Asp Cys Ile Asp Gly Ser Asp Glu Leu Met Cys Glu Ile Thr
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4237
    Lys Pro Pro Ser Asp Asp Ser Pro Ala His Ser Ser Ala Ile Gly Pro
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    gtc att ggc atc atc ctc tct ctc ttc gtc atg ggt ggt gtc tat ttt
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    Val Ile Gly Ile Ile Leu Ser Leu Phe Val Met Gly Gly Val Tyr Phe
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4333
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    ttc ccg cac gag tat gtc agc ggg acc ccg cac gtg ccc ctc aat ttc
4381
    Phe Pro His Glu Tyr Val Ser Gly Thr Pro His Val Pro Leu Asn Phe
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    ata gcc ccg ggc ggt tcc cag cat ggc ccc ttc aca ggc atc gca tgc
4429
    Ile Ala Pro Gly Gly Ser Gln His Gly Pro Phe Thr Gly Ile Ala Cys
          1440          1445          1450
    gga aag tcc atg atg agc tcc gtg agc ctg atg ggg ggc cgg ggc ggg
4477
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4525
    Val Pro Leu Tyr Asp Arg Asn His Val Thr Gly Ala Ser Ser Ser Ser
          1470          1475          1480          1485
    tcg tcc agc acg aag gcc acg ctg tac ccg ccg atc ctg aac ccg ccg
4573
    Ser Ser Ser Thr Lys Ala Thr Leu Tyr Pro Pro Ile Leu Asn Pro Pro
          1490          1495          1500
    ccc tcc ccg gcc acg gac ccc tcc ctg tac aac atg gac atg ttc tac
4621
    Pro Ser Pro Ala Thr Asp Pro Ser Leu Tyr Asn Met Asp Met Phe Tyr
          1505          1510          1515
    tct tca aac att ccg gcc act gcg aga ccg tac agg ccc tac atc att
4669
    Ser Ser Asn Ile Pro Ala Thr Ala Arg Pro Tyr Arg Pro Tyr Ile Ile
          1520          1525          1530
    cga gga atg gcg ccc ccg acg acg ccc tgc agc acc gac gtg tgt gac
4717
    Arg Gly Met Ala Pro Pro Thr Thr Pro Cys Ser Thr Asp Val Cys Asp
          1535          1540          1545
    agc gac tac agc gcc agc cgc tgg aag gcc agc aag tac tac ctg gat
4765
    Ser Asp Tyr Ser Ala Ser Arg Trp Lys Ala Ser Lys Tyr Tyr Leu Asp
          1550          1555          1560          1565
    ttg aac tcg gac tca gac ccc tat cca ccc cca ccc acg ccc cac agc
4813
    Leu Asn Ser Asp Ser Asp Pro Tyr Pro Pro Pro Pro Thr Pro His Ser
          1570          1575          1580

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 Gln Tyr Leu Ser Ala Glu Asp Ser Cys Pro Pro Ser Pro Ala Thr Glu
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 4909
 Arg Ser Tyr Phe His Leu Phe Pro Pro Pro Pro Ser Pro Cys Thr Asp
 1600 1605 1610
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 4965
 Ser Ser
 1615
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 5025
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 35 40 45
 Gly Gly Val Lys Leu Glu Ser Thr Ile Val Val Ser Gly Leu Glu Asp
 50 55 60
 Ala Ala Ala Val Asp Phe Gln Phe Ser Lys Gly Ala Val Tyr Trp Thr
 65 70 75 80
 Asp Val Ser Glu Glu Ala Ile Lys Gln Thr Tyr Leu Asn Gln Thr Gly
 85 90 95
 Ala Ala Val Gln Asn Val Val Ile Ser Gly Leu Val Ser Pro Asp Gly
 100 105 110
 Leu Ala Cys Asp Trp Val Gly Lys Lys Leu Tyr Trp Thr Asp Ser Glu
 115 120 125
 Thr Asn Arg Ile Glu Val Ala Asn Leu Asn Gly Thr Ser Arg Lys Val
 130 135 140
 Leu Phe Trp Gln Asp Leu Asp Gln Pro Lys Ala Ile Ala Leu Asp Pro
 145 150 155 160
 Ala His Gly Tyr Met Tyr Trp Thr Asp Trp Gly Glu Thr Pro Arg Ile
 165 170 175
 Glu Arg Ala Gly Met Asp Gly Ser Thr Arg Lys Ile Ile Val Asp Ser
 180 185 190
 Asp Ile Tyr Trp Pro Asn Gly Leu Thr Ile Asp Leu Glu Glu Gln Lys
 195 200 205
 Leu Tyr Trp Ala Asp Ala Lys Leu Ser Phe Ile His Arg Ala Asn Leu
 210 215 220
 Asp Gly Ser Phe Arg Gln Lys Val Val Glu Gly Ser Leu Thr His Pro
 225 230 235 240
 Phe Ala Leu Thr Leu Ser Gly Asp Thr Leu Tyr Trp Thr Asp Trp Gln
 245 250 255

Thr	Arg	Ser	Ile	His	Ala	Cys	Asn	Lys	Arg	Thr	Gly	Gly	Lys	Arg	Lys
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Glu	Ile	Leu	Ser	Ala	Leu	Tyr	Ser	Pro	Met	Asp	Ile	Gln	Val	Leu	Ser
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Gln	Glu	Arg	Gln	Pro	Phe	Phe	His	Thr	Arg	Cys	Glu	Glu	Asp	Asn	Gly
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Cys	Ala	Cys	Pro	Thr	Gly	Val	Gln	Met	Gln	Asp	Asn	Gly	Arg	Thr	Cys
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Lys	Ala	Gly	Ala	Glu	Glu	Val	Leu	Leu	Leu	Ala	Arg	Arg	Thr	Asp	Leu
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Arg	Arg	Ile	Ser	Leu	Asp	Thr	Pro	Asp	Phe	Thr	Asp	Ile	Val	Leu	Gln
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Val	Asp	Asp	Ile	Arg	His	Ala	Ile	Ala	Ile	Asp	Tyr	Asp	Pro	Leu	Glu
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Tyr	Leu	Asp	Gly	Ser	Gly	Ala	Gln	Thr	Leu	Val	Asn	Thr	Glu	Ile	Asn
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Asp	Pro	Asp	Gly	Ile	Ala	Val	Asp	Trp	Val	Ala	Arg	Asn	Leu	Tyr	Trp
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Asn	Pro	Lys	Ile	Glu	Cys	Ala	Asn	Leu	Asp	Gly	Gln	Glu	Arg	Arg	Val
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Leu	Val	Asn	Ala	Ser	Leu	Gly	Trp	Pro	Asn	Gly	Leu	Ala	Leu	Asp	Leu
			500					505					510		
Gln	Glu	Gly	Lys	Leu	Tyr	Trp	Gly	Asp	Ala	Lys	Thr	Asp	Lys	Ile	Glu
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Val	Ile	Asn	Val	Asp	Gly	Thr	Lys	Arg	Arg	Thr	Leu	Leu	Glu	Asp	Lys
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Leu	Pro	His	Ile	Phe	Gly	Phe	Thr	Leu	Leu	Gly	Asp	Phe	Ile	Tyr	Trp
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Thr	Asp	Trp	Gln	Arg	Arg	Ser	Ile	Glu	Arg	Val	His	Lys	Val	Lys	Ala
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Ser	Arg	Asp	Val	Ile	Ile	Asp	Gln	Leu	Pro	Asp	Leu	Met	Gly	Leu	Lys
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Ala	Val	Asn	Val	Ala	Lys	Val	Val	Gly	Thr	Asn	Pro	Cys	Ala	Asp	Arg
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Asn	Gly	Gly	Cys	Ser	His	Leu	Cys	Phe	Phe	Thr	Pro	His	Ala	Thr	Arg
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Cys	Gly	Cys	Pro	Ile	Gly	Leu	Glu	Leu	Leu	Ser	Asp	Met	Lys	Thr	Cys
625					630					635					640
Ile	Val	Pro	Glu	Ala	Phe	Leu	Val	Phe	Thr	Ser	Arg	Ala	Ala	Ile	His
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Arg	Ile	Ser	Leu	Glu	Thr	Asn	Asn	Asn	Asp	Val	Ala	Ile	Pro	Leu	Thr
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Leu	Ile	Gln	Gly	His	Leu	Asp	Phe	Val	Met	Asp	Ile	Leu	Val	Phe	His
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Thr	Asp	Thr	Gly	Thr	Asp	Arg	Ile	Glu	Val	Thr	Arg	Leu	Asn	Gly	Thr	
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Ser	Arg	Lys	Ile	Leu	Val	Ser	Glu	Asp	Leu	Asp	Glu	Pro	Arg	Ala	Ile	
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Gly	Val	Lys	Glu	Ala	Ser	Ala	Leu	Asp	Phe	Asp	Val	Ser	Asn	Asn	His	
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Glu	Gly	Met	Ala	Val	Asp	Trp	Met	Gly	Lys	Asn	Leu	Tyr	Trp	Ala	Asp	
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Asp	Lys	Val	Gly	Arg	Ala	Asn	Asp	Leu	Thr	Ile	Asp	Tyr	Ala	Asp	Gln	
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Leu Ile Gln Gly His Leu Asp Phe Val Met Asp Ile Leu Val Phe His		880
	885	890
Ser Ser Arg Gln Asp Gly Leu Asn Asp Cys Met His Asn Asn Gly Gln		895
	900	905
Cys Gly Gln Leu Cys Leu Ala Ile Pro Gly Gly His Arg Cys Gly Cys		910
	915	920
Ala Ser His Tyr Thr Leu Asp Pro Ser Ser Arg Asn Cys Ser Pro Pro		925
	930	935
Thr Thr Phe Leu Leu Phe Ser Gln Lys Ser Ala Ile Ser Arg Met Ile		940
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Pro Asp Asp Gln His Ser Pro Asp Leu Ile Leu Pro Leu His Gly Leu		960
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Arg Asn Val Lys Ala Ile Asp Tyr Asp Pro Leu Asp Lys Phe Ile Tyr		975
	980	985
Trp Val Asp Gly Arg Gln Asn Ile Lys Arg Ala Lys Asp Asp Gly Thr		990
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Gln Pro Phe Val Leu Thr Ser Leu Ser Gln Gly Gln Asn Pro Asp Arg		1005
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Gln Pro His Asp Leu Ser Ile Asp Ile Tyr Ser Arg Thr Leu Phe Trp		1020
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Arg Ala Ala Lys Ile Glu Arg Ala Ala Leu Asp Gly Thr Glu Arg Glu		1085
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Val Leu Phe Thr Thr Gly Leu Ile Arg Pro Val Ala Leu Val Val Asp		1100
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Glu Ser Cys Asp Leu Ser Gly Ala Asn Arg Leu Thr Leu Glu Asp Ala		1135
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Ala Cys Ala Thr Gly Glu Ile Asp Cys Ile Pro Gly Ala Trp Arg Cys		1260
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Val Cys Ser Ala Ala Gln Phe Pro Cys Ala Arg Gly Gln Cys Val Asp		1295
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 cacggaccgc atcgagggtga cgcgcctcaa cggcacctcc cgcaagatcc tgggtgtcga 360
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<400> 47
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 gccgcagcat cgagcgggtg cacaagggtca aggccagccg ggacgtcatc attgaccagc 180
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244

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<212> DNA

<213> Homo sapiens

<400> 48

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tgaagacctg	catcgtgcct	gaggcctttt	tggctcttcac	cagcagagcc	gccatccaca	180
ggatctccct	cgagaccaat	aacaacgacg	tggccatccc	gctcacgggc	gtcaaggagg	240
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<210> 49

<211> 255

<212> DNA

<213> Homo sapiens

<400> 49

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gggcccagac	tgggaccaac	agaatcgaag	tggcgcggct	ggacgggcag	ttccggcaag	180
tcctcgtgtg	gagggacttg	gacaacccga	ggtcgctggc	cctggatccc	accaaggggt	240
aagtgtttgc	ctgtc					255

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<211> 210

<212> DNA

<213> Homo sapiens

<400> 50

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accattgact	acgctgacca	gcgcctctac	tggaccgacc	tggacaccaa	catgatcgag	180
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<211> 352

<212> DNA

<213> Homo sapiens

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ccgacaagac	tagcggccgg	aaccgcaccc	tcattccagg	ccacctggac	ttcgtgatgg	180
acatcctggg	gttccactcc	tcccggccagg	atggcctcaa	tgactgtatg	cacaacaacg	240
ggcagtgtgg	gcagctgtgc	cttgccatcc	ccggcggcca	ccgctgcggc	tgcgcctcac	300
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<211> 225

<212> DNA

<213> Homo sapiens

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aaagccatcg	actatgacct	actggacaag	ttcatctact	gggtggatgg	gcgccagaac	180
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caataccatc	aacgtccaca	ggctgagcgg	ggaagccatg	gggtgggtgc	tgcgtgggga	180
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cgcgcagccc	tggacggcac	cgagcgcgag	gtcctcttca	ccaccggcct	catccgccct	120
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 <211> 234
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gtgtggagaa	gaccaccggg	gacaagcgga	ctcgcattcca	gggccgtgtc	gcccacctca	180
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cacaggggag	atcgactgta	tccccggggc	ctggcgctgt	gacggctttc	ccgagtgcga	120
tgaccagagc	gacgaggagg	gctgccccgt	gtgctccgcc	gcccagttcc	cctgcgcgcg	180

gggtcagtg	gtggacctgc	gcctgcgctg	cgacggcgag	gcagactgtc	aggaccgctc	240
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tgtgccagcg	cgtgggtgtg	cagcgctatg	cgggggccaa	cgggcccttc	ccgcacgagt	180
atgtcagcgg	gaccccgcac	gtgcccctca	atttcatagc	cccgggcggg	tcccagcatg	240
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<210> 60
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gccagcaagt	actacctgga	tttgaactcg	gactcagacc	cctatccacc	cccaccacg	180
ccccacagcc	agtacctgtc	ggcggaggac	agctgcccgc	cctcgcccgc	caccgagagg	240
agctacttcc	atctcttccc	gccccctccg	tccccctgca	cggactcatc	ctgacctcgg	300
cggggccact	ctggcttctc	tgtgcccctg	taaatagttt	taaatatgaa	caaagaaaaa	360

aatatat	atgtt	taaaa	aaataaatat	aattgggatt	ttaaaaaacat	gagaaatgtg	420
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<220>
 <223> Artificial Sequence is a primer.

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<220>
 <223> Artificial Sequence is a primer.

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